

#8
OICE

RAW SEQUENCE LISTING

DATE: 08/16/2001

PATENT APPLICATION: US/09/817,913

TIME: 13:08:27

Input Set : A:\106101-145.ST25.txt

Output Set: N:\CRF3\08162001\I817913.raw

ENTERED

P. 5

ENTERED

5 <110> APPLICANT: Li, Zuomei
 6 Bonfils, Claire
 7 Besterman, Jeffrey
 9 <120> TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
 11 <130> FILE REFERENCE: 106101.145
 13 <140> CURRENT APPLICATION NUMBER: US 09/817,913
 14 <141> CURRENT FILING DATE: 2001-03-26
 16 <150> PRIOR APPLICATION NUMBER: US 60/192,157
 17 <151> PRIOR FILING DATE: 2000-03-24
 19 <160> NUMBER OF SEQ ID NOS: 33
 21 <170> SOFTWARE: PatentIn version 3.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 481
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Human
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 39 35 40 45
 42 Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Asn Ala Glu Glu Met
 43 50 55 60
 46 Thr Lys Tyr His Ser Asp Tyr Ile Lys Phe Leu Arg Ser Ile Arg
 47 65 70 75 80
 50 Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met Gln Arg Phe Asn Val
 51 85 90 95
 54 Gly Glu Asp Cys Pro Val Phe Asp Gly Leu Phe Glu Phe Cys Gln Leu
 55 100 105 110
 58 Ser Thr Gly Gly Ser Val Ala Ser Ala Val Lys Leu Asn Lys Gln Gln
 59 115 120 125
 62 Thr Asp Ile Ala Val Asn Trp Ala Gly Gly Leu His His Ala Lys Lys
 63 130 135 140
 66 Ser Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile Val Leu Ala Ile
 67 145 150 155 160
 70 Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr Ile Asp Ile Asp
 71 165 170 175
 74 Ile His His Gly Asp Gly Val Glu Glu Ala Phe Tyr Thr Thr Asp Arg
 75 180 185 190
 78 Val Met Thr Val Ser Phe His Lys Tyr Gly Glu Tyr Phe Pro Gly Thr
 79 195 200 205
 82 Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr Tyr Ala Val
 83 210 215 220
 86 Tyr Pro Leu Arg Asp Gly Ile Asp Asp Glu Ser Tyr Glu Ala Ile Phe
 87 225 230 235 240
 90 Lys Pro Val Met Ser Lys Val Met Glu Met Phe Gln Pro Ser Ala Val

Non-enclosed
check
diskette

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94 Val Leu Gln Cys Gly Ser Asp Ser Leu Ser Gly Asp Arg Leu Gly Cys
95          260          265          270
98 Phe Asn Leu Thr Ile Lys Gly His Ala Lys Cys Val Glu Phe Val Lys
99          275          280          285
102 Ser Phe Asn Leu Pro Met Leu Met Leu Gly Gly Gly Gly Tyr Thr Ile
103          290          295          300
106 Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr Ala Val Ala Leu Asp
107 305          310          315          320
110 Thr Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp Tyr Phe Glu Tyr Phe
111          325          330          335
114 Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser Asn Met Thr Asn Gln
115          340          345          350
118 Asn Thr Asn Glu Tyr Leu Glu Lys Ile Lys Gln Arg Leu Phe Glu Asn
119          355          360          365
122 Leu Arg Met Leu Pro His Ala Pro Gly Val Gln Met Gln Ala Ile Pro
123          370          375          380
126 Glu Asp Ala Ile Pro Glu Glu Ser Gly Asp Glu Asp Glu Asp Asp Pro
127 385          390          395          400
130 Asp Lys Arg Ile Ser Ile Cys Ser Ser Asp Lys Arg Ile Ala Cys Glu
131          405          410          415
134 Glu Glu Phe Ser Asp Ser Glu Glu Glu Gly Glu Gly Gly Arg Lys Asn
135          420          425          430
138 Ser Ser Asn Phe Lys Lys Ala Lys Arg Val Lys Thr Glu Asp Glu Lys
139          435          440          445
142 Glu Lys Asp Pro Glu Glu Lys Lys Glu Val Thr Glu Glu Glu Lys Thr
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156 <211> LENGTH: 1611

157 <212> TYPE: DNA

158 <213> ORGANISM: Human

160 <400> SEQUENCE: 2

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165 cgcaggcac ccggaggaaa gtctgttact actacgacgg ggatgttgga aattactatt      180
167 atggacaagg ccaccaatg aagcctcacc gaatccgcac gactcataat ttgctgctca      240
169 actatggtct ctaccgaaaa atggaaatct atcgccctca caaagccaat gctgaggaga      300
171 tgaccaagta ccacagcgat gactacatta aattcttgcg ctccatccgt ccagataaca      360
173 tgtcggagta cagcaagcag atgcagagat tcaacgttgg tgaggactgt ccagtattcg      420
175 atggcctgtt tgagttctgt cagttgtcta ctggtggttc tgtggcaagt gctgtgaaac      480
177 ttaataagca gcagacggac atcgccgtga attgggctgg gggcctgcac catgcaaaga      540
179 agtccgaggc atctggcttc tgttacgtca atgatatcgt cttggccatc ctggaactgc      600
181 taaagtatca ccagaggggtg ctgtacattg acattgatat tcaccatggt gacggcgtgg      660
183 aagaggcctt ctacaccacg gaccgggtca tgactgtgtc ctttcataag tatggagagt      720
185 acttcccagg aactggggac ctacgggata ccggggctgg caaagacaag tattatgctg      780
187 ttaactaccc gctccgagac gggattgatg acgagtccta tgaggccatt ttcaagccgg      840

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189 tcatgtccaa agtaatggag atgttccagc ctagtgcggt ggtcttacag tgtggctcag      900
191 actccctatc tggggatcgg ttaggttgct tcaatctatc tatcaaagga cagccaagt      960
193 gtgtggaatt tgtcaagagc tttaacctgc ctatgctgat gctgggaggc ggtggttaca    1020
195 ccattcgtaa cgttgcccgg tgctggacat atgagacagc tgtggccctg gatacggaga    1080
197 tccctaataga gcttccatac aatgactact ttgaatactt tggaccagat ttcaagctcc    1140
199 acatcagttcc ttccaatatg actaaccaga acacgaatga gtacctggag aagatcaaac    1200
201 agcgactggt tgagaacctt agaatgctgc cgcacgcacc tggggtccaa acgcaggcga    1260
203 ttcctgagga cgccatccct gaggagagtg gcgatgagga cgaagacgac cctgacaagc    1320
205 gcatctcgat ctgctcctct gacaaacgaa ttgctgtga ggaagagttc tccgattctg    1380
207 aagaggaggg agaggggggc cgcaagaact cttccaactt caaaaaagcc aagagagtca    1440
209 aaacagagga tgaaaaagag aaagaccagc aggagaagaa aggaatcacc gaagaggaga    1500
211 aaaccaagga ggagaagcca gaagccaaag gggtaagga ggaggccaag ttggcctgaa    1560
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218 <211> LENGTH: 489
219 <212> TYPE: PRT
220 <213> ORGANISM: Human
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228 Tyr Tyr Asp Gly Asp Ile Gly Asn Tyr Tyr Tyr Gly Gln Gly His Pro
229 20 25 30
232 Met Lys Pro His Arg Ile Arg Met Thr His Asn Leu Leu Leu Asn Tyr
233 35 40 45
236 Gly Leu Tyr Arg Lys Met Glu Ile Tyr Arg Pro His Lys Ala Thr Ala
237 50 55 60
240 Glu Glu Met Thr Lys Tyr His Ser Asp Glu Tyr Ile Lys Phe Leu Arg
241 65 70 75 80
244 Ser Ile Arg Pro Asp Asn Met Ser Glu Tyr Ser Lys Gln Met His Ile
245 85 90 95
248 Pro Phe Asn Val Gly Glu Asp Cys Pro Ala Phe Asp Gly Leu Phe Glu
249 100 105 110
252 Phe Cys Gln Leu Ser Thr Gly Gly Ser Val Ala Gly Ala Val Lys Leu
253 115 120 125
256 Asn Arg Gln Gln Thr Asp Met Ala Val Asn Trp Ala Gly Gly Leu His
257 130 135 140
260 His Ala Lys Lys Tyr Glu Ala Ser Gly Phe Cys Tyr Val Asn Asp Ile
261 145 150 155 160
264 Val Leu Ala Ile Leu Glu Leu Leu Lys Tyr His Gln Arg Val Leu Tyr
265 165 170 175
268 Ile Asp Ile Asp Ile His His Arg Gly Asp Gly Val Glu Glu Ala Phe
269 180 185 190
272 Tyr Thr Thr Asp Arg Val Met Thr Val Ser Phe Tyr Gly Glu Tyr Phe
273 195 200 205
276 Pro Gly Thr Gly Asp Leu Arg Asp Ile Gly Ala Gly Lys Gly Lys Tyr
277 210 215 220
280 Tyr Ala Val Asn Phe Pro Met Cys Asp Gly Ile Asp Asp Glu Ser Tyr
281 225 230 235 240
284 Gly Gln Ile Phe Lys Pro Ile Ile Ser Lys Val Met Glu Met Tyr Gln

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| 285 | 245 | 250 | 255 |
| 288 Pro Ser Ala Val Val Leu Gln Cys Gly Ala Asp Ser Leu Ser Gly Asp | | | |
| 289 | 260 | 265 | 270 |
| 292 Arg Leu Gly Cys Phe Asn Leu Thr Val Lys Gly His Ala Lys Cys Val | | | |
| 293 | 275 | 280 | 285 |
| 296 Glu Val Val Lys Thr Phe Asn Leu Pro Leu Leu Met Leu Gly Gly Gly | | | |
| 297 | 290 | 295 | 300 |
| 300 Gly Tyr Thr Ile Leu Arg Asn Val Ala Arg Cys Trp Thr Tyr Glu Thr | | | |
| 301 305 | 310 | 315 | 320 |
| 304 Ala Val Ala Leu Asp Cys Glu Ile Pro Asn Glu Leu Pro Tyr Asn Asp | | | |
| 305 | 325 | 330 | 335 |
| 308 Tyr Phe Glu Tyr Phe Gly Pro Asp Phe Lys Leu His Ile Ser Pro Ser | | | |
| 309 | 340 | 345 | 350 |
| 312 Asn Met Thr Asn Gln Asn Thr Pro Glu Tyr Met Glu Lys Ile Lys Gln | | | |
| 313 | 355 | 360 | 365 |
| 316 Arg Leu Phe Glu Asn Leu Arg Met Leu Pro His Ala Pro Gly Val Gln | | | |
| 317 | 370 | 375 | 380 |
| 320 Met Gln Ala Ile Pro Glu Asp Ala Val His Glu Asp Ser Gly Asp Glu | | | |
| 321 385 | 390 | 395 | 400 |
| 324 Asp Gly Glu Asp Pro Asp Lys Arg Ile Ser Ile Arg Ala Ser Asp Lys | | | |
| 325 | 405 | 410 | 415 |
| 328 Arg Ile Ala Cys Asp Glu Glu Phe Ser Asp Ser Glu Asp Glu Gly Glu | | | |
| 329 | 420 | 425 | 430 |
| 332 Gly Gly Arg Asn Val Ala Asp His Lys Lys Gly Ala Lys Ala Arg Ile | | | |
| 333 | 435 | 440 | 445 |
| 336 Glu Glu Asp Lys Lys Glu Thr Glu Asp Lys Lys Thr Asp Val Lys Glu | | | |
| 337 | 450 | 455 | 460 |
| 340 Glu Asp Lys Ser Lys Asp Asn Ser Gly Glu Lys Thr Asp Thr Lys Gly | | | |
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| 357 ctcccaccgg cctgcccttc cccgcgggac tatcgcccc acgtttccct cagccctttt | 120 | | |
| 359 ctctcccggc cgagccgcgg cggcagcagc agcagcagca gcagcaggag gaggagcccg | 180 | | |
| 361 gtggcgggcg tggcggggga gcccatggcg tacagtcaag gaggcggcaa aaaaaaagtc | 240 | | |
| 363 tgctactact acgacggtga tattggaaat tattattatg gacaggggtca tcccatgaag | 300 | | |
| 365 cctcatagaa tccgcatgac ccataacttg ctgttaaatt atggcttaca cagaaaaatg | 360 | | |
| 367 gaaatatata ggccccataa agccactgcc gaagaaatga caaaatatca cagtgatgag | 420 | | |
| 369 tatatcaaat ttctacgggc aataagacca gataacatgt ctgagtatag taagcagatg | 480 | | |
| 371 catatattta atgttgagaga agattgtcca gcgtttgatg gactctttga gttttgtcag | 540 | | |
| 373 ctctcaactg gcggttcagt tgctggagct gtgaagttaa accgacaaca gactgatatg | 600 | | |
| 375 gctgttaatt gggctggagg attacatcat gctaagaaat acgaagcatc aggatcctgt | 660 | | |
| 377 tacgttaatg atattgtgct tgccatcctt gaattactaa agtatcatca gagagtctta | 720 | | |
| 379 tatatcgata tagatattca tcatggtgat ggtgtcgaag aagcttttta tacaacagat | 780 | | |

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381 cgtgtaatga cggatcatt ccataaatat ggggaatact ttcctggcac aggagacttg      840
383 agggatattg gtgctggaag aggcaaatac tatgctgtca attttccaat gtgtgatgg      900
385 atagacgatg agtcatatgg gcagatatatt aagcctatta tctcaaagggt gatggagatg      960
387 tatcaacctg gtgctgtggg attacagtgt ggtgcagact cattatctgg tgatagactg     1020
389 ggttggtttca atctaacagt caaagggtcat gctaaatgtg tagaagttgt aaaaactttt     1080
391 aactttacat tactgatgct tggaggagggt ggctacacaa tccgtaatgt tgctcgatgt     1140
393 tggacatatg agactgcagt tgcccttgat tgtgagattc ccaacgagtt gccatataat     1200
395 gattactttg agtatttttg accagacttc aaactgcata ttagtccttc aaacatgaca     1260
397 aaccagaaca ctccagaata tacggaaaag ataaaacagc gtttggttga aaatttgccg     1320
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401 gacagtggag atgaagatgg agaagatcca gacaagagaa tttctattcg agcatcagac     1440
403 aagcggatag cttgtgatga agaattctca gattctgagg atgaaggaga aggaggtcga     1500
405 agaaatgtgg ctgatcataa gaaaggagca aagaaagcta gaattgaaga agataagaaa     1560
407 gaaacagagg acaaaaaaac agacgttaag gaagaagata aatccaagga caacagtggg     1620
409 gaaaaaacag ataccaaagg aaccaaatac gaacagctca gcaacccctg aatctgacag     1680
411 tctaccaaat ttcagaaaat cattaataaag aaaatattga aaggaaaatg ttttcttttt     1740
413 gaagactttc ggcttcattt tatactactt tggcatggac tgtatttatt ttcaaattgg     1800
415 actttttcgt ttttggtttt ctgggcaagt tttattgtga gattttctaa ttatgaagca     1860
417 aaattttctt tctccaccat gctttatgtg atagtattta aaattgatgt gagttattat     1920
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427 <212> TYPE: PRT
428 <213> ORGANISM: Human
430 <400> SEQUENCE: 5

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437          20          25          30
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441          35          40          45
444 Lys Pro Tyr Gln Ala Ser Gln His Asp Met Cys Arg Phe His Ser Glu
445          50          55          60
448 Asp Tyr Ile Asp Phe Leu Gln Arg Val Ser Pro Thr Asn Met Gln Gly
449 65          70          75          80
452 Phe Thr Lys Ser Leu Asn Ala Pro Asn Val Gly Asp Asp Cys Pro Val
453          85          90          95
456 Phe Pro Gly Leu Phe Glu Phe Cys Ser Arg Tyr Thr Gly Ala Ser Leu
457          100         105         110
460 Gln Gly Ala Thr Gln Leu Asn Asn Lys Ile Cys Asp Ile Ala Asn Trp
461          115         120         125
464 Ala Gly Gly Leu His His Ala Lys Lys Phe Glu Ala Ser Gly Phe Cys
465          130         135         140
468 Tyr Val Asn Asp Ile Val Ile Gly Ile Leu Glu Leu Leu Leu Lys Tyr
469 145          150         155         160
472 His Pro Arg Val Leu Tyr Ile Asp Ile Asp Ile His His Gly Asp Gly
473          165         170         175
476 Val Gln Glu Ala Phe Tyr Leu Thr Asp Arg Val Met Thr Val Ser Phe

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Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:2337 M:283 W: Missing Blank Line separator, <220> field identifier
L:2398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:2400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16